What is claimed:

1. A method for amplifying a nucleic acid sample from blood comprising:

providing a nucleic acid sample from blood;

hybridizing at least one reduction oligonucleotide to at least one unwanted RNA in the sample;

incubating the mixture with an RNase H and subsequently inactivating the RNase H;

hybridizing a primer comprising oligo dT to the RNA in the mixture;

extending the primer to make cDNA; and

amplifying the cDNA.

2. The method of claim 1 wherein the unwanted RNA comprises a poly(A) tail and wherein the reduction oligonucleotide hybridizes to the unwanted RNA in the region of the unwanted RNA that is near the 5' end of the poly(A) tail of the unwanted RNA.

3. The method of claim 1 wherein the RNase H is inactivated by depleting RNase H from the mixture.

4. The method of claim 1 wherein the RNase H is thermolabile and inactivation is by heating.

5. The method of claim 1 wherein the RNase H is inactivated by addition of EDTA to the mixture.

6. The method of claim 1 wherein the RNase H is inactivated by separating the RNase H from the nucleic acid by organic extraction.

7. The method of claim 1 wherein the RNase H is removed by separating the RNA from the RNase H by column purification.

8. The method of claim 1 wherein the primer further comprises a RNA polymerase promoter sequence.

9. The method of claim 8 wherein the step of amplifying the cDNA comprises making double stranded cDNA comprising a functional RNA polymerase promoter region and synthesizing multiple copies of RNA from the double stranded cDNA using an RNA polymerase.

10. The method of claim 1 wherein the unwanted nucleic acid is a globin mRNA.

11. The method of claim 1 wherein the unwanted nucleic acid is selected from the group consisting of alpha-1 globin, alpha-2 globin and beta globin.

12. The method of claim 10 wherein a plurality of different species of reduction oligonucleotides are used and each species is complementary to a globin mRNA.

13. The method of claim 1 wherein after hybridizing the reduction oligonucleotide to the unwanted mRNA, the reduction oligonucleotide is extended by a polymerase.

14. The method of claim 1 wherein after incubating the mixture with RNase H the reduction oligonucleotide is removed.

15. The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 1.

16. The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 2.

17. The method of claim 1 wherein the at least one reduction oligonucleotide consists essentially of SEQ ID NO 3.

18. The method of claim 1 wherein a mixture of different sequence reduction oligonuclotides are added to the mixture.

19. The method of claim 18 wherein the mixture comprises SEQ ID NOs 1, 2 and 3.

20. The method of claim 1 wherein said nucleic acid sample from blood is obtained from blood that was collected in a container containing an RNA stabilizing agent.

21. The method of claim 20 wherein said RNA stabilizing agent is selected from the group consisting of cationic compounds, detergents, chaotropic salts, ribonuclease inhibitors, chelating agents, and mixtures thereof.

22. The method of claim 20 wherein said RNA stabilizing agent is selected from the group consisting of phenol, chloroform, acetone, alcohols and mixtures thereof.

23. The method of claim 20 wherein said nucleic acid sample from blood is obtained from blood that was collected in a container containing a RNA stabilizing agent and wherein said RNA stabilizing agent is selected from the group consisting of mercapto-alcohols, di-thio-threitol (DTT), and mixtures thereof.

24. A method for analyzing a nucleic acid sample isolated from blood comprising:

a. providing a first nucleic acid sample;
b. blocking amplification of unwanted nucleic acid sequences in the nucleic acid sample by hybridizing a reduction oligonucleotide to said unwanted nucleic acid sequences to form a RNA:DNA hybrid and digesting the RNA:DNA hybrid;
c. amplifying unblocked nucleic acid sequences to produce an amplified nucleic acid sample;
d. contacting said amplified nucleic acid sample with a solid support comprising nucleic acid probes to generate a hybridization pattern; and
e. analyzing the hybridization pattern.

25. The method of claim 24, further comprising: detecting the presence or absence of hybridization of said amplified nucleic acid sample to said nucleic acid probes on said solid support.

26. The method of claim 24, further comprising: labeling said amplified nucleic acid sample.

27. The method of claim 24 wherein said unwanted nucleic acid sequences are repetitive sequences.

28. The method of claim 24 wherein said unblocked nucleic acid sequences are non-specifically amplified by in vitro transcription.

29. The method of claim 24 wherein said unwanted nucleic acid sequences are globin mRNAs.

30. The method of claim 29 wherein said globin mRNAs are greater than 20% of the first nucleic acid sample and wherein said globin mRNAs are less than 20% of the amplified nucleic acid sample.

31. A method for amplifying a nucleic acid sample from blood comprising:

providing a nucleic acid sample from blood;

hybridizing at least one reduction oligonucleotide to at least one unwanted RNA in the sample generating reduction oligonucleotide:unwanted RNA complexes;

removing the reduction oligonucleotide:unwanted RNA complexes from the sample; and,

amplifying at least one target RNA remaining in the sample.

32. The method of claim 31 wherein reduction oligonucleotide:unwanted RNA complexes are removed from the sample by affinity purification.

33. The method of claim 31 wherein said reduction oligonucleotide comprises biotin and said reduction oligonucleotide:unwanted RNA complexes are removed from the sample by hybridization to a solid support.

34. The method of claim 33 wherein said solid support comprises streptavidin.

35. The method of claim 31 wherein the RNA is amplified by mixing with random primers, extending the random primers to make cDNA and labeling the cDNA.

36. The method of claim 35 wherein the labeled cDNA is hybridized to a solid support and the hybridization pattern is analyzed.